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Fig. 1:

	1	56
I16 human	MnsFStsaFgPVAFsLGLLLVLpaAFPapvppgeDskDvaapPhRQpLTsSErIDkq	
I16 mouse	MkFLSaRdFhPVAF.LGLMLVttTAFPtqvrgDftEdttPnRpVytSQ.VGgl	
I16 hhv8	McWFk1WsL....L1VGsLLVsgT.....RGkLpDapefeKDLLi.....qr	
Consensus	*	* * *
	57	112
I16 human	IrYILDgIsaLRKEtCNKsnMCeSskEALAENNlnLPkMaEkDGCFQsGFNEETCL	
I16 mouse	IthVLWeIvEMRKELCNgnSdCmnndDALAENNlKLPeIqrnDGCYQtGYNQEiCL	
I16 hhv8	LnWMLWvIdEcfrDLCyRtGICKGilepaAifhLKLPaInDtDhCgliGFNETsCL	
Consensus	*	* * * * * * * * * * * *
	113	168
I16 human	VKIitGLLEFEVYLEYLqNrF.EsSeEqARaVQMstKvLIQFLQkkaKNLdaIttP	
I16 mouse	LKIissGLLEYhsYLEYmkNnLkDnkkDkARVLQrdTeTLIHFnQEVKDLhKIVlp	
I16 hhv8	kKLadGFFEFEV1FkFLtteF.GkSvinvdVMELLTKTLgwdIQEELnkLtKthys	
Consensus	*	* * *
	169	223
I16 human	dPttNASLLtKLQAQnQWLqdmTtHLILRSFkeFLqssLRalRQM.....	
I16 mouse	tPisNA1LtDKLESQKEWLRtkTiQFILKSLEEFLKvtLRstRQt.....	
I16 hhv8	pPkfDrGLLGRLQGlKyWVRhfasfYVLsaMEkFagqaVRvLdsIpdvtpdvhdk.	
Consensus	*	* * * * * * *

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Fig. 2:

SEQUENCE LISTING

1. Sequence characteristics:

1.1.	Length:	612 base pairs
1.2.	Type:	Nucleic Acid
1.3.	Strandedness:	Double stranded
1.4.	Topology:	Linear
2.	Molecule type:	Genomic DNA
3.	Description:	Human herpesvirus 8 interleukin-6 gene
4.	Hypothetical:	No
5.	Anti-sense:	No
6.	Original source:	Kaposi Sarkoma from HIV positive donor
7.	Organism:	Human herpesvirus 8

1 ATG TGC TGG TTC AAG TTG TGG TCT CTC TTG CTG GTC GGT TCA CTG
1 M C W F K L W S L L L V G S L
1 Met Cys Trp Phe Lys Leu Trp Ser Leu Leu Leu Val Gly Ser Leu

46 CTG GTA TCT GGA ACG CGG GGC AAG TTG CCG GAC GCC CCC GAG TTT
16 L V S G T R G K L P D A P E F
16 Leu Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe

91 GAA AAG GAT CTT CTC ATT CAG AGA CTC AAT TGG ATG CTA TGG GTG
31 E K D L L I Q R L N W M L W V
31 Glu Lys Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val

136 ATC GAT GAA TGC TTC CGC GAC CTC TGT TAC CGT ACC GGC ATC TGC
46 I D E C F R D L C Y R T G I C
46 Ile Asp Glu Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys

181 AAG GGT ATT CTA GAG CCC GCT GCT ATT TTT CAT CTG AAA CTA CCA
61 K G I L E P A A I F H L K L P
61 Lys Gly Ile Leu Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro

226 GCC ATC AAC GAT ACT GAT CAC TGC GGG TTA ATA GGA TTT AAT GAG
76 A I N D T D H C G L I G F N E
76 Ala Ile Asn Asp Thr Asp His Cys Gly Leu Ile Gly Phe Asn Glu

271 ACT AGC TGC CTT AAA AAG CTC GCC GAT GGC TTT TTT GAA TTC GAG
91 T S C L K K L A D G F F E F E
91 Thr Ser Cys Leu Lys Leu Ala Asp Gly Phe Phe Glu Phe Glu

316 GTG TTG TTT AAG TTT TTA ACG ACG GAG TTT GGA AAA TCA GTG ATA
106 V L F K F L T T E F G K S V I
106 Val Leu Phe Lys Phe Leu Thr Thr Glu Phe Gly Lys Ser Val Ile

361 AAC GTG GAC GTC ATG GAG CTT CTG ACG AAG ACC TTA GGA TGG GAC
121 N V D V M E L L T K T L G W D
121 Asn Val Asp Val Met Glu Leu Leu Thr Lys Thr Leu Gly Trp Asp

406 ATA CAG GAA GAG CTC AAT AAG CTG ACT AAG ACG CAC TAC AGT CCA
136 I Q E E L N K L T K T H Y S P
136 Ile Gln Glu Glu Leu Asn Lys Leu Thr Lys Thr His Tyr Ser Pro

451 CCC AAA TTT GAC CGC GGT CTA TTA GGG AGG CTT CAG GGA CTT AAG
151 P K F D R G L L G R L Q G L K
151 Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg Leu Gln Gly Leu Lys

496 TAT TGG GTG AGA CAC TTT GCT TCG TTT TAT GTT CTG AGT GCA ATG
166 Y W V R H F A S F Y V L S A M
166 Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val Leu Ser Ala Met

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541 GAA AAG TTT GCA GGT CAA GCG GTG CGT GTT TTG GAC TCT ATC CCA
181 E K F A G Q A V R V L D S I P
181 Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp Ser Ile Pro

586 GAC GTG ACT CCT GAC GTC CAC GAT AAG
196 D V T P D V H D K
196 Asp Val Thr Pro Asp Val His Asp Lys